

# The impact of habitual diet on the human gut microbiome.

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## Introduction

Dietary regulation of the gut microbiota on a person-by-person basis could be crucial to disease treatment. Current research provides a general grasp of the effect of diet on the composition and activity of the gut microbiota, but precise information of how to use diet as a tool is still lacking. Due to the field's relative freshness, methodologies have yet to be standardised, resulting in widely diverse study outputs. This could be due to variables relating to the difficulties in accurately representing both nutrition and the gut microbiota. The intricacy and existing methodology of diet-microbial relationships are discussed in this review, as well as the implications and limitations of these investigative approaches, as well as future considerations that may aid in expediting applications [1].

## The Gut Microbiome

The human gut microbiome is made up of commensal microorganisms such as bacteria, viruses, fungus, and protozoa that live in the human intestine. Bacteria are the well-studied of them, and they will be the subject of this review. Gram positive Firmicutes and gram negative Bacteroidetes are the most common bacterial groups in the microbiome. Recently, it was discovered that the microbiota can be separated into various enterotypes, each of which is enriched by different bacterial species but all of which appear to have excellent functional homogeneity. This homogeneity exists regardless of host characteristics such as age, gender, BMI, and nationality.

The bulk of bacteria live in the digestive tracts most distal regions, where their biomass exceeds 10<sup>11</sup> cells per gram. Microbes in the distal gut contribute to the health of the host by biosynthesising vitamins and critical amino acids, as well as producing important metabolic by products from dietary components that the small intestine has not digested. Short chain fatty acids (SCFA) found in products like butyrate, propionate, and acetate serve as a primary source of energy for intestinal epithelial cells, potentially strengthening the mucosal barrier. Moreover, studies using germ-free mice suggest that the microbiota directly promotes local intestinal immunity by affecting TLR expression, antigen presenting cells, differentiated T cells, and lymphoid follicles, as well as systemic immunity by increasing splenic CD4<sup>+</sup> T cells and systemic antibody expression [2].

These and other documented benefits have sparked increased interest in the capacity to alter the gut microbiota. Within 24 hours of starting a new diet—for example, switching to a completely animal-based or plant-based diet—microbial composition changes, and within 48 hours of stopping the diet, the microbial composition returns to baseline. Furthermore, animals fed a high-fat or high-sugar diet have a gut microbiome

that is more susceptible to circadian rhythm disruption. Overwhelming systemic stress and inflammation, such as that generated by severe burn injury, has also been shown to cause typical acute changes in the gut microbiota within one day after the prolonged insult, according to studies.

## Diet and Microbiota

### Protein

Dietary protein's effects on the gut flora were first documented in 1977. In a culture-based investigation, participants who ate a heavy beef diet had lower numbers of Bifidobacterium adolescents and higher counts of Bacteroides and Clostridia than those who ate a meatless diet. Several researches have been able to extensively evaluate the impact of dietary protein on gut bacteria composition thanks to advancements in 16S rRNA sequencing. In this research, participants were given a variety of protein sources, including high animal-based protein from meats, eggs, and cheeses, whey protein, and totally vegetarian sources such pea protein. Protein consumption is found to be favourably correlated with overall microbial diversity in the majority of investigations. For example, consumption of whey and pea protein extract has been reported to increase gut-commensal Bifidobacterium and Lactobacillus, while whey additionally decreases the pathogenic Bacteroides fragilis and Clostridium perfringens [3].

Pea protein has also been shown to raise intestinal SCFA levels, which are anti-inflammatory and crucial for the mucosal barrier's maintenance. On the contrary, consumption of animal-based protein increased the number of bile-tolerant anaerobes such as Bacteroides, Alistipes, and Basophil. An independent study comparing the microbiota of Italian youngsters to that of children in a rural African village backs up this claim. Bacteroides and Alistipes were shown to be more abundant in the microbiota of Italian youngsters who ate more animal protein.

### Fats

Diets high in saturated and trans fats are known to raise the risk of cardiovascular disease by raising total and LDL cholesterol levels in the blood. Health-promoting fats, such as mono and polyunsaturated fats, on the other hand, are critical in reducing the risk of chronic disease. Because the normal Western diet is high in saturated and trans fats yet deficient in mono and polyunsaturated fats, frequent consumers are predisposed to a variety of health concerns. A high-fat diet has been shown in several human studies to enhance overall anaerobic microbiota and Bacteroides numbers [4].

Subjects were given diets with variable fat content to examine the impact of different types of dietary fat on human gut flora.

The scientists found that following a low-fat diet resulted in higher faecal Bifidobacterium abundance, as well as lower fasting glucose and total cholesterol levels, as compared to baseline. A high saturated fat diet, on the other hand, increased the amount of faecal bacterium prausnitzii. Finally, patients who consumed a lot of monounsaturated fat did not have any changes in the relative abundance of any bacterial species, but they did have a lower total bacterial load and lower total and LDL cholesterol in their blood [5].

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